



SEQUENCE LISTING

Anderson et al.

<120> CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE (MURI)

<130> ASZD-P01-007

<140> 10/729,571

<141> 2003-12-05

<150> 60/435,272

<151> 2002-12-20

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<151> 2002-12-20

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<151> 2002-12-20

<160> 76

<170> PatentIn version 3.1

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<211> 768

<212> DNA

<213> H. pylori

<221> CDS

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| atg | aaa | ata | ggc | gtt | ttt | gat | agc | ggt | gtg | ggg | ggg | ttt | agc | gtt | tta | 48 |
| Met | Lys | Ile | Gly | Val | Phe | Asp | Ser | Gly | Val | Gly | Gly | Phe | Ser | Val | Leu | |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| aaa | agc | ctt | tta | aaa | gcg | cga | ttg | ttt | gat | gaa | atc | atc | tac | tat | ggc | 96 |
| Lys | Ser | Leu | Leu | Lys | Ala | Arg | Leu | Phe | Asp | Glu | Ile | Ile | Tyr | Tyr | Gly | |
| | | 20 | | | | | 25 | | | | | | 30 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gat | agc | gct | aga | gtg | cct | tat | ggc | act | aaa | gac | ccc | acc | acg | atc | aag | 144 |
| Asp | Ser | Ala | Arg | Val | Pro | Tyr | Gly | Thr | Lys | Asp | Pro | Thr | Thr | Ile | Lys | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| caa | ttt | ggc | tta | gag | gct | ttg | gat | ttt | ttc | aaa | ccg | cat | gag | att | gaa | 192 |
| Gln | Phe | Gly | Leu | Glu | Ala | Leu | Asp | Phe | Phe | Lys | Pro | His | Glu | Ile | Glu | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | ttg | att | gtg | gca | tgc | aac | acc | gcg | agc | gct | ctg | gct | tta | gaa | gag | 240 |
| Leu | Leu | Ile | Val | Ala | Cys | Asn | Thr | Ala | Ser | Ala | Leu | Ala | Leu | Glu | Glu | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | caa | aag | tat | tct | aaa | atc | cct | att | gtg | ggc | gtg | att | gag | cca | agc | 288 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Met | Gln | Lys | Tyr | Ser | Lys | Ile | Pro | Ile | Val | Gly | Val | Ile | Glu | Pro | Ser | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| att | tta | gcg | atc | aag | cgg | caa | gtg | gaa | gat | aaa | aac | gcc | cct | att | tta | | 336 |
| Ile | Leu | Ala | Ile | Lys | Arg | Gln | Val | Glu | Asp | Lys | Asn | Ala | Pro | Ile | Leu | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| gtg | cta | ggg | aca | aaa | gcg | acg | att | caa | tcc | aac | gcc | tat | gac | aac | gcc | | 384 |
| Val | Leu | Gly | Thr | Lys | Ala | Thr | Ile | Gln | Ser | Asn | Ala | Tyr | Asp | Asn | Ala | | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| ctg | aaa | caa | caa | ggc | tat | ttg | aac | att | tcg | cat | tta | gct | act | tct | ctt | | 432 |
| Leu | Lys | Gln | Gln | Gly | Tyr | Leu | Asn | Ile | Ser | His | Leu | Ala | Thr | Ser | Leu | | |
| | 130 | | | | | | 135 | | | | | 140 | | | | | |
| ttt | gtg | cct | ttg | att | gaa | gaa | agt | att | tta | gag | ggc | gaa | ttg | tta | gaa | | 480 |
| Phe | Val | Pro | Leu | Ile | Glu | Glu | Ser | Ile | Leu | Glu | Gly | Glu | Leu | Leu | Glu | | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | | |
| act | tgc | atg | cat | tat | tat | ttc | act | ccc | tta | gag | att | tta | ccc | gaa | gtg | | 528 |
| Thr | Cys | Met | His | Tyr | Tyr | Phe | Thr | Pro | Leu | Glu | Ile | Leu | Pro | Glu | Val | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| atc | att | tta | ggt | tgc | acg | cat | ttt | ccc | tta | atc | gct | caa | aaa | att | gag | | 576 |
| Ile | Ile | Leu | Gly | Cys | Thr | His | Phe | Pro | Leu | Ile | Ala | Gln | Lys | Ile | Glu | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| ggc | tat | ttc | atg | ggg | cat | ttt | gcc | ctt | cca | acg | ccc | ccc | cta | ctc | atc | | 624 |
| Gly | Tyr | Phe | Met | Gly | His | Phe | Ala | Leu | Pro | Thr | Pro | Pro | Leu | Leu | Ile | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| cat | tcg | ggc | gat | gct | att | gta | gaa | tat | ttg | caa | caa | aaa | tac | gcc | ctt | | 672 |
| His | Ser | Gly | Asp | Ala | Ile | Val | Glu | Tyr | Leu | Gln | Gln | Lys | Tyr | Ala | Leu | | |
| | | 210 | | | | 215 | | | | | 220 | | | | | | |
| aaa | aac | aat | gca | tgc | aca | ttc | cct | aaa | gtg | gaa | ttt | cat | gcg | agc | ggc | | 720 |
| Lys | Asn | Asn | Ala | Cys | Thr | Phe | Pro | Lys | Val | Glu | Phe | His | Ala | Ser | Gly | | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | | |
| gat | gtg | atc | tgg | cta | gaa | aga | caa | gct | aaa | gaa | tgg | ctc | aaa | ttg | taa | | 768 |
| Asp | Val | Ile | Trp | Leu | Glu | Arg | Gln | Ala | Lys | Glu | Trp | Leu | Lys | Leu | | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |

<210> 2
 <211> 255
 <212> PRT
 <213> H. pylori

<400> 2

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Lys | Ile | Gly | Val | Phe | Asp | Ser | Gly | Val | Gly | Gly | Phe | Ser | Val | Leu | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Lys | Ser | Leu | Leu | Lys | Ala | Arg | Leu | Phe | Asp | Glu | Ile | Ile | Tyr | Tyr | Gly | | |
| | | 20 | | | | | | 25 | | | | | 30 | | | | |

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu
 50 55 60
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80
 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95
 Ile Leu Ala Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu
 100 105 110
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125
 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
 130 135 140
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160
 Thr Cys Met His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190
 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
 195 200 205
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220
 Lys Asn Asn Ala Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240
 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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<221> CDS
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<400> 3

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| atg aaa ata ggc gtt ttt gat agc ggt gtg ggg ggg ttt agc gtt tta | 48 |
| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | |
| 1 5 10 15 | |
| aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc | 96 |
| Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly | |
| 20 25 30 | |
| gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag | 144 |
| Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys | |
| 35 40 45 | |
| caa ttt ggc tta gag gct ttg gat ttt ttc aaa cca cac cag att gaa | 192 |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu | |
| 50 55 60 | |
| tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag | 240 |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | |
| 65 70 75 80 | |
| atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc | 288 |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | |
| 85 90 95 | |
| att tta gcg atc aag caa caa gtg aaa gat aaa aac gcc cct att tta | 336 |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | |
| 100 105 110 | |
| gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc | 384 |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | |
| 115 120 125 | |
| ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt | 432 |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu | |
| 130 135 140 | |
| ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag | 480 |
| Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu | |
| 145 150 155 160 | |
| act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg | 528 |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val | |
| 165 170 175 | |
| att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag | 576 |
| Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu | |
| 180 185 190 | |
| ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc | 624 |

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
 195 200 205

cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac gcc ctt 672
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

aaa aac aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa 768
 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 4
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Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
245 250 255

<210> 5

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<222> (1)..(768)

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| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | |
| 1 5 10 15 | |
| aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc | 96 |
| Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly | |
| 20 25 30 | |
| gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag | 144 |
| Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys | |
| 35 40 45 | |
| caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa | 192 |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu | |
| 50 55 60 | |
| tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag | 240 |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | |
| 65 70 75 80 | |

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

att tta gcg atc aag cga caa gta aaa gat aaa aac gcc cct att tta 336
 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aat gcc 384
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa 480
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc gaa gtg 528
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
 165 170 175

att att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

ggc tat ttt atg gag cat ttt gcc ctt tca aca ccc ccc cta ctc atc 624
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

cat tcg ggc gat gct att gta gga tat ttg cag caa aaa tac gcc ctt 672
 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa 768
 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 6
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 <212> PRT
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<400> 6

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys.
35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
245 250 255

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<221> CDS
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| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | |
| 1 5 10 15 | |
| aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc | 96 |
| Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly | |
| 20 25 30 | |
| gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag | 144 |
| Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys | |
| 35 40 45 | |
| caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa | 192 |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys | |
| 50 55 60 | |
| tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag | 240 |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | |
| 65 70 75 80 | |
| atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc | 288 |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | |
| 85 90 95 | |
| att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta | 336 |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | |
| 100 105 110 | |
| gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aac gcc | 384 |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | |
| 115 120 125 | |
| ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt | 432 |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu | |
| 130 135 140 | |
| ttt gtg cct ttg att gaa gaa agt att tta ggg ggc gaa ttg tta gaa | 480 |
| Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Gly Gly Glu Leu Leu Glu | |
| 145 150 155 160 | |
| act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg | 528 |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val | |
| 165 170 175 | |
| att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag | 576 |
| Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu | |
| 180 185 190 | |

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt 672
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

gat gtg atc tgg cta gaa aaa cag gct aa 749
 Asp Val Ile Trp Leu Glu Lys Gln Ala
 245

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Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Gly Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala
245

<210> 9

<211> 768

<212> DNA

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<221> CDS

<222> (1)..(768)

<400> 9

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Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1 5 10 15

aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc 96
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
20 25 30

gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga 192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
50 55 60

tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc 288
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

att tta gcg atc aag caa caa gta aaa gat aaa aac gcc tct att ttg 336
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Ser Ile Leu
 100 105 110

gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aac gcc 384
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa 480
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

act tgc atg cgt tat tat ttc act ccg tta gag atc ttg cct gaa gtg 528
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

gtt att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576
 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt 672
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc 720
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768
 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 10
 <211> 255
 <212> PRT
 <213> H. pylori

<400> 10

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly

| | | |
|--|----|----|
| 20 | 25 | 30 |
| Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys 35 40 45 | | |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly 50 55 60 | | |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu 65 70 75 80 | | |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser 85 90 95 | | |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Ser Ile Leu 100 105 110 | | |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala 115 120 125 | | |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu 130 135 140 | | |
| Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu 145 150 155 160 | | |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val 165 170 175 | | |
| Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu 180 185 190 | | |
| Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile 195 200 205 | | |
| His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu 210 215 220 | | |
| Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly 225 230 235 240 | | |
| Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu 245 250 255 | | |

<210> 11
 <211> 749
 <212> DNA
 <213> H. pylori

<221> CDS
 <222> (1)..(747)

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 1 5 10 15
 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60
 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80
 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95
 att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta 336
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110
 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc 384
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125
 cta aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt 432
 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
 130 135 140
 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag 480
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160
 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg 528
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
 165 170 175
 atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag 576
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

ggc tat ttt atg gag cat ttt gcc ctt cca acc ccc ccc cta ctc atc 624
Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
195 200 205

cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac acc ctt 672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
210 215 220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc 720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

gat gtg gtt tgg cta gaa aaa cag gct aa 749
Asp Val Val Trp Leu Glu Lys Gln Ala
245

| | |
|-------|-----------|
| <210> | 12 |
| <211> | 249 |
| <212> | PRT |
| <213> | H. pylori |

<400> 12

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu

130 135 140
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
 165 170 175
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190
 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
 195 200 205
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
 210 215 220
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240
 Asp Val Val Trp Leu Glu Lys Gln Ala
 245

<210> 13
 <211> 768
 <212> DNA
 <213> H. pylori

<221> CDS
 <222> (1)..(768)

<400> 13
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 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15
 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30
 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
 50 55 60
 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu

| 65 | 70 | 75 | 80 | |
|---|-----|-----|-----|-----|
| atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc | | | | 288 |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | | | | |
| | 85 | 90 | 95 | |
| att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta | | | | 336 |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | | | | |
| | 100 | 105 | 110 | |
| gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gcc | | | | 384 |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | | | | |
| | 115 | 120 | 125 | |
| ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt | | | | 432 |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu | | | | |
| | 130 | 135 | 140 | |
| ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa | | | | 480 |
| Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu | | | | |
| | 145 | 150 | 155 | 160 |
| act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg | | | | 528 |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val | | | | |
| | 165 | 170 | 175 | |
| atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag | | | | 576 |
| Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu | | | | |
| | 180 | 185 | 190 | |
| ggc tat ttt atg gag cat ttt gcc ctt tta acg ccc ccc cta ctc atc | | | | 624 |
| Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile | | | | |
| | 195 | 200 | 205 | |
| cat tct ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt | | | | 672 |
| His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu | | | | |
| | 210 | 215 | 220 | |
| aag aaa aat gca cac tca ttc cct aaa gtg gaa ttt cat gcg agc gcc | | | | 720 |
| Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly | | | | |
| | 225 | 230 | 235 | 240 |
| gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa | | | | 768 |
| Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu | | | | |
| | 245 | 250 | 255 | |
| <210> 14 | | | | |
| <211> 255 | | | | |
| <212> PRT | | | | |
| <213> H. pylori | | | | |
| <400> 14 | | | | |
| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | | | | |
| 1 | 5 | 10 | 15 | |

Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
210 215 220

Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly
225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu

| | 245 | 250 | 255 | |
|---|------------------|-----|-----|-----|
| <210> | 15 | | | |
| <211> | 768 | | | |
| <212> | DNA | | | |
| <213> | <i>H. pylori</i> | | | |
| <221> | CDS | | | |
| <222> | (1)..(768) | | | |
| <400> | 15 | | | |
| atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta | | | | 48 |
| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | | | | |
| 1 5 10 15 | | | | |
| aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc | | | | 96 |
| Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly | | | | |
| 20 25 30 | | | | |
| gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag | | | | 144 |
| Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys | | | | |
| 35 40 45 | | | | |
| caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa | | | | 192 |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu | | | | |
| 50 55 60 | | | | |
| tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag | | | | 240 |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | | | | |
| 65 70 75 80 | | | | |
| atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc | | | | 288 |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | | | | |
| 85 90 95 | | | | |
| att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta | | | | 336 |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | | | | |
| 100 105 110 | | | | |
| gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gac aac gcc | | | | 384 |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | | | | |
| 115 120 125 | | | | |
| ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt | | | | 432 |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu | | | | |
| 130 135 140 | | | | |
| ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa | | | | 480 |
| Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu | | | | |
| 145 150 155 160 | | | | |
| act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc aaa gta | | | | 528 |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val | | | | |
| 165 170 175 | | | | |
| atc att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att aag | | | | 576 |
| Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys | | | | |

| | | | |
|---|-----|-----|-----|
| 180 | 185 | 190 | |
| ggc tat ttt atg ggg cat ttt gcc ctt tca acg ccc ccc cta ctc atc | | | 624 |
| Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile | | | |
| 195 | 200 | 205 | |
| cat tcg ggc gat gct att gtg gga tat ttg caa caa aaa tac gcc ctt | | | 672 |
| His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu | | | |
| 210 | 215 | 220 | |
| aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc | | | 720 |
| Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly | | | |
| 225 | 230 | 235 | 240 |
| gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa | | | 768 |
| Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu | | | |
| 245 | 250 | 255 | |
| | | | |
| <210> 16 | | | |
| <211> 255 | | | |
| <212> PRT | | | |
| <213> H. pylori | | | |
| | | | |
| <400> 16 | | | |
| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | | | |
| 1 | 5 | 10 | 15 |
| Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly | | | |
| 20 | 25 | 30 | |
| Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys | | | |
| 35 | 40 | 45 | |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu | | | |
| 50 | 55 | 60 | |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | | | |
| 65 | 70 | 75 | 80 |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | | | |
| 85 | 90 | 95 | |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | | | |
| 100 | 105 | 110 | |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | | | |
| 115 | 120 | 125 | |

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys
 180 185 190

Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 17
 <211> 768
 <212> DNA
 <213> H. pylori

<221> CDS
 <222> (1)..(768)

<400> 17
 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta 48
 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15
 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60
 tta ttg att gtg gca tgc aac aca gcg agt gct ctg gct tta gaa gag 240

| | | | | | | | | | | | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Ile | Val | Ala | Cys | Asn | Thr | Ala | Ser | Ala | Leu | Ala | Leu | Glu | Glu | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| <i>atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc</i> | | | | | | | | | | | | | | | | | |
| Met | Gln | Lys | His | Ser | Lys | Ile | Pro | Ile | Val | Gly | Val | Ile | Glu | Pro | Ser | | 288 |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| <i>att tta gcg atc aaa caa cag gta aaa gat aaa aac gcc ccc att tta</i> | | | | | | | | | | | | | | | | | |
| Ile | Leu | Ala | Ile | Lys | Gln | Gln | Val | Lys | Asp | Lys | Asn | Ala | Pro | Ile | Leu | | 336 |
| | | | | 100 | | | | 105 | | | | | 110 | | | | |
| <i>gtg cta ggc aca aaa gcg acg att caa tct aac gct tac gat aac gct</i> | | | | | | | | | | | | | | | | | |
| Val | Leu | Gly | Thr | Lys | Ala | Thr | Ile | Gln | Ser | Asn | Ala | Tyr | Asp | Asn | Ala | | 384 |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| <i>ctg aaa cga caa ggc tat ttg aac gtt tcg cat tta gcc act tcc ctt</i> | | | | | | | | | | | | | | | | | |
| Leu | Lys | Arg | Gln | Gly | Tyr | Leu | Asn | Val | Ser | His | Leu | Ala | Thr | Ser | Leu | | 432 |
| | | 130 | | | | 135 | | | | | 140 | | | | | | |
| <i>ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa</i> | | | | | | | | | | | | | | | | | |
| Phe | Val | Pro | Leu | Ile | Glu | Glu | Ser | Ile | Leu | Glu | Gly | Glu | Leu | Leu | Glu | | 480 |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| <i>act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg</i> | | | | | | | | | | | | | | | | | |
| Thr | Cys | Met | Arg | Tyr | Tyr | Phe | Thr | Pro | Leu | Lys | Ile | Leu | Pro | Glu | Val | | 528 |
| | | | | 165 | | | | 170 | | | | | | 175 | | | |
| <i>atc att tta ggt tgt acg cat ttt ccc ttg atc gct caa aaa att gag</i> | | | | | | | | | | | | | | | | | |
| Ile | Ile | Leu | Gly | Cys | Thr | His | Phe | Pro | Leu | Ile | Ala | Gln | Lys | Ile | Glu | | 576 |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| <i>ggc tat ttt atg gaa cat ttt gcc ttt cca acg ccc ccc cta ctc atc</i> | | | | | | | | | | | | | | | | | |
| Gly | Tyr | Phe | Met | Glu | His | Phe | Ala | Phe | Pro | Thr | Pro | Pro | Pro | Leu | Leu | Ile | 624 |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| <i>cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt</i> | | | | | | | | | | | | | | | | | |
| His | Ser | Gly | Asp | Ala | Ile | Val | Glu | Tyr | Leu | Gln | Gln | Lys | Tyr | Ala | Leu | | 672 |
| | | 210 | | | | 215 | | | | 220 | | | | | | | |
| <i>aag aaa aat gca cac gca tta cct aaa gtg gaa ttt cat gcg agc ggc</i> | | | | | | | | | | | | | | | | | |
| Lys | Lys | Asn | Ala | His | Ala | Leu | Pro | Lys | Val | Glu | Phe | His | Ala | Ser | Gly | | 720 |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| <i>gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa</i> | | | | | | | | | | | | | | | | | |
| Asp | Val | Ile | Trp | Leu | Glu | Lys | Gln | Ala | Lys | Glu | Trp | Leu | Lys | Leu | | | 768 |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| <210> 18 <211> 255 <212> PRT <213> H. pylori <400> 18 | | | | | | | | | | | | | | | | | |
| Met | Lys | Ile | Gly | Val | Phe | Asp | Ser | Gly | Val | Gly | Gly | Phe | Ser | Val | Leu | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |

Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Arg Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Phe Pro Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala His Ala Leu Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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 <213> H. pylori

<221> CDS
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 1 5 10 15

aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

att tta gcg atc aaa caa caa gta aag gat aaa aac gcc ccc att tta 336
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gct 384
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt 432
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa 480
 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

act tgc atg cgt tat tat ttc act ccc tta gag att tta cct gaa gtg 528
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc ata ctc atc 624
 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
 195 200 205

cat tct ggc gac gct att gta gaa tat ttg caa caa aaa tac gcc ctt 672
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

gat atg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa 768
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 245 250 255

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 <211> 255
 <212> PRT
 <213> H. pylori

<400> 20

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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Met Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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 <213> H. pylori

<221> CDS
 <222> (1)..(768)

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 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
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 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

| | |
|---|-----|
| tta ttg att gta gca tgc aac aca gcg agc gct cta gct tta gaa gag | 240 |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | |
| 65 70 75 80 | |
| atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc | 288 |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | |
| 85 90 95 | |
| att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta | 336 |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | |
| 100 105 110 | |
| gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc | 384 |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | |
| 115 120 125 | |
| ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt | 432 |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu | |
| 130 135 140 | |
| ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa | 480 |
| Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu | |
| 145 150 155 160 | |
| act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg | 528 |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val | |
| 165 170 175 | |
| att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag | 576 |
| Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu | |
| 180 185 190 | |
| agc tat ttt atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc | 624 |
| Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile | |
| 195 200 205 | |
| cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt | 672 |
| His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu | |
| 210 215 220 | |
| aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc | 720 |
| Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly | |
| 225 230 235 240 | |
| gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa | 768 |
| Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu | |
| 245 250 255 | |
| <210> 22 | |
| <211> 255 | |
| <212> PRT | |
| <213> H. pylori | |
| <400> 22 | |
| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | |
| 1 5 10 15 | |

Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 23
 <211> 768
 <212> DNA
 <213> H. pylori

<221> CDS
 <222> (1)..(768)

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 1 5 10 15

aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
 50 55 60

tta ttg att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag 240
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

atg caa aaa tat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc ccc att tta 336
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

gtg cta ggg aca aaa gcg acg atc caa tct aac gct tat gat aac gcc 384
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

ctg aaa caa caa ggc tat ttg aac att tgc cat tta gcc act tct ctt 432
 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
 130 135 140

ttt gtg ccc ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa 480
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg 528
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag 576
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

agc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc 624
 Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

cat tct ggc gat gct att gtg gaa tac ttg caa caa aaa tac gcc ctt 672
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768
 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 24
 <211> 255
 <212> PRT
 <213> H. pylori

<400> 24

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala

115

120

125

Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 25
 <211> 768
 <212> DNA
 <213> H. pylori

<221> CDS
 <222> (1)..(768)

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 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15
 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aaa att gaa 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu

| 50 | 55 | 60 | |
|---|-----|-----|-----|
| tta tta att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag | | | 240 |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | | | |
| 65 | 70 | 75 | 80 |
| atg caa aag cat tcc aaa atc ccc att gtg ggc gtg att gag cca agc | | | 288 |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | | | |
| | 85 | 90 | 95 |
| att tta gcg atc aaa caa caa gtg aaa gat aaa aac acc cct att tta | | | 336 |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Thr Pro Ile Leu | | | |
| | 100 | 105 | 110 |
| gtg cta ggg aca aaa gcg acg atc caa tct aac gct tac gat aac gcc | | | 384 |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | | | |
| | 115 | 120 | 125 |
| ctg aaa caa caa ggc tat ttg aag gtt tcg cat ttg gcc act tct ctt | | | 432 |
| Leu Lys Gln Gln Gly Tyr Leu Lys Val Ser His Leu Ala Thr Ser Leu | | | |
| | 130 | 135 | 140 |
| ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa | | | 480 |
| Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu | | | |
| | 145 | 150 | 155 |
| act tgc atg cgt tat tat ttc act cca tta gaa atc tta cct gaa gtg | | | 528 |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val | | | |
| | 165 | 170 | 175 |
| gtt att tta ggc tgc acg cat ttt ccc ttg atc gct caa aaa att gag | | | 576 |
| Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu | | | |
| | 180 | 185 | 190 |
| ggc tat ttt atg gaa cat ttt gcc ctt cca acg ccc ccc cta ctc atc | | | 624 |
| Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile | | | |
| | 195 | 200 | 205 |
| cat tct ggc gac gct att gtg gga tat ttg cag caa aaa tac gcc ctt | | | 672 |
| His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu | | | |
| | 210 | 215 | 220 |
| aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc | | | 720 |
| Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly | | | |
| | 225 | 230 | 235 |
| gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa | | | 768 |
| Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu | | | |
| | 245 | 250 | 255 |

<210> 26

<211> 255

<212> PRT

<213> H. pylori

<400> 26

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Thr Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Lys Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly

| | | | | |
|---|---------------------|-------------------------|-----|-----|
| 225 | 230 | 235 | 240 | |
| Asp Val Ile Trp | Leu Glu Lys Gln Ala | Lys Glu Trp Leu Lys Leu | | |
| | 245 | 250 | 255 | |
| <210> 27 | | | | |
| <211> 768 | | | | |
| <212> DNA | | | | |
| <213> H. pylori | | | | |
| <221> CDS | | | | |
| <222> (1)..(768) | | | | |
| <400> 27 | | | | |
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| Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu | | | | |
| 1 | 5 | 10 | 15 | |
| aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc | | | | |
| Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly | | | | 96 |
| | 20 | 25 | 30 | |
| gat agc gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag | | | | |
| Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys | | | | 144 |
| | 35 | 40 | 45 | |
| caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa | | | | |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu | | | | 192 |
| | 50 | 55 | 60 | |
| tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gaa | | | | |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | | | | 240 |
| | 65 | 70 | 75 | 80 |
| atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc | | | | |
| Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser | | | | 288 |
| | 85 | 90 | 95 | |
| att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta | | | | |
| Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | | | | 336 |
| | 100 | 105 | 110 | |
| gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc | | | | |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | | | | 384 |
| | 115 | 120 | 125 | |
| ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt | | | | |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu | | | | 432 |
| | 130 | 135 | 140 | |
| ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa | | | | |
| Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu | | | | 480 |
| | 145 | 150 | 155 | 160 |
| act tgc atg cgt tat tat ttc act cca tta gag atc ttg cct gaa gtg | | | | |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val | | | | 528 |

| 165 | | | | | | | | | | 170 | | | | | 175 | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| gtt | att | tta | ggc | tgc | acg | cat | ttt | ccc | ttg | atc | gct | cac | caa | att | gag | 576 | | | | |
| Val | Ile | Leu | Gly | Cys | Thr | His | Phe | Pro | Leu | Ile | Ala | His | Gln | Ile | Glu | | | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | | | |
| ggc | tat | ttt | atg | gag | cat | ttt | gcc | ctt | tca | acg | ccc | ccc | cta | ctc | atc | 624 | | | | |
| Gly | Tyr | Phe | Met | Glu | His | Phe | Ala | Leu | Ser | Thr | Pro | Pro | Leu | Leu | Ile | | | | | |
| | | 195 | | | | | 200 | | | | 205 | | | | | | | | | |
| cat | tct | ggc | gat | gct | att | gtg | gaa | tat | ttg | cag | caa | aaa | tac | gcc | ctt | 672 | | | | |
| His | Ser | Gly | Asp | Ala | Ile | Val | Glu | Tyr | Leu | Gln | Gln | Lys | Tyr | Ala | Leu | | | | | |
| | 210 | | | | | 215 | | | | 220 | | | | | | | | | | |
| aag | aaa | aac | gca | tgt | gca | ttc | cct | aaa | gta | gaa | ttt | cat | gcg | agc | ggc | 720 | | | | |
| Lys | Lys | Asn | Ala | Cys | Ala | Phe | Pro | Lys | Val | Glu | Phe | His | Ala | Ser | Gly | | | | | |
| 225 | | | | | 230 | | | | 235 | | | | | | 240 | | | | | |
| gat | gta | att | tgg | cta | gaa | aaa | cag | gct | aaa | gaa | tgg | ctc | aaa | ttg | taa | 768 | | | | |
| Asp | Val | Ile | Trp | Leu | Glu | Lys | Gln | Ala | Lys | Glu | Trp | Leu | Lys | Leu | | | | | | |
| | | | 245 | | | | | 250 | | | | | 255 | | | | | | | |
| <210> 28 | | | | | | | | | | | | | | | | | | | | |
| <211> 255 | | | | | | | | | | | | | | | | | | | | |
| <212> PRT | | | | | | | | | | | | | | | | | | | | |
| <213> H. pylori | | | | | | | | | | | | | | | | | | | | |
| <400> 28 | | | | | | | | | | | | | | | | | | | | |
| Met | Lys | Ile | Gly | Val | Phe | Asp | Ser | Gly | Val | Gly | Gly | Phe | Ser | Val | Leu | | | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | | | |
| Lys | Ser | Leu | Leu | Lys | Ala | Gln | Ile | Phe | Asp | Glu | Ile | Ile | Tyr | Tyr | Gly | | | | | |
| | | 20 | | | | | | 25 | | | | | 30 | | | | | | | |
| Asp | Ser | Ala | Arg | Val | Pro | Tyr | Gly | Thr | Lys | Asp | Pro | Thr | Thr | Ile | Lys | | | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | | | |
| Gln | Phe | Gly | Leu | Glu | Ala | Leu | Asp | Phe | Phe | Lys | Pro | His | Lys | Ile | Glu | | | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | | | |
| Leu | Leu | Ile | Val | Ala | Cys | Asn | Thr | Ala | Ser | Ala | Leu | Ala | Leu | Glu | Glu | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | | | |
| Met | Gln | Lys | His | Ser | Lys | Ile | Pro | Ile | Val | Gly | Val | Ile | Glu | Pro | Ser | | | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | | | |
| Ile | Leu | Ala | Ile | Lys | Gln | Gln | Val | Lys | Asp | Lys | Asn | Ala | Pro | Ile | Leu | | | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | | | |

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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 <213> H. pylori

<221> CDS
 <222> (1)..(768)

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 1 5 10 15
 aaa agc ctt tta aaa gtg caa tta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30
 gat agt gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa 192

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Phe | Gly | Leu | Glu | Ala | Leu | Asp | Phe | Phe | Lys | Pro | His | Lys | Ile | Glu | | |
| 50 | | | | | | 55 | | | | | 60 | | | | | | |
| tta | ttg | att | gtg | gca | tgc | aac | aca | gcg | agc | gct | cta | gct | tta | gga | gag | 240 | |
| Leu | Leu | Ile | Val | Ala | Cys | Asn | Thr | Ala | Ser | Ala | Leu | Ala | Leu | Gly | Glu | | |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | | | |
| atg | caa | aag | tat | tcc | aaa | atc | cct | att | gtg | ggc | gtg | att | gag | cca | agc | 288 | |
| Met | Gln | Lys | Tyr | Ser | Lys | Ile | Pro | Ile | Val | Gly | Val | Ile | Glu | Pro | Ser | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| att | tta | gcg | atc | aaa | caa | caa | gta | aaa | gat | aaa | aac | gcc | cct | att | tta | 336 | |
| Ile | Leu | Ala | Ile | Lys | Gln | Gln | Val | Lys | Asp | Lys | Asn | Ala | Pro | Ile | Leu | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| gta | cta | ggg | aca | aaa | gcg | acg | att | cga | tcc | aac | gct | tat | gac | aac | gcc | 384 | |
| Val | Leu | Gly | Thr | Lys | Ala | Thr | Ile | Arg | Ser | Asn | Ala | Tyr | Asp | Asn | Ala | | |
| | | | 115 | | | | 120 | | | | | | 125 | | | | |
| ctg | aaa | caa | caa | ggc | tat | ttg | aat | att | tcg | cat | tta | gcc | act | tct | ctt | 432 | |
| Leu | Lys | Gln | Gln | Gly | Tyr | Leu | Asn | Ile | Ser | His | Leu | Ala | Thr | Ser | Leu | | |
| | | | 130 | | | | 135 | | | | | 140 | | | | | |
| ttt | gtg | cct | ttg | att | gaa | gaa | aat | att | tta | gag | ggc | gaa | ttg | cta | gaa | 480 | |
| Phe | Val | Pro | Leu | Ile | Glu | Glu | Asn | Ile | Leu | Glu | Gly | Glu | Leu | Leu | Glu | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| act | tgc | atg | cgt | tat | tat | ttc | act | cca | tta | gag | att | tta | cct | gaa | gtg | 528 | |
| Thr | Cys | Met | Arg | Tyr | Tyr | Phe | Thr | Pro | Leu | Glu | Ile | Leu | Pro | Glu | Val | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| gtt | att | tta | ggt | tgc | acg | cat | ttt | ccc | ttg | atc | gct | cac | caa | att | gag | 576 | |
| Val | Ile | Leu | Gly | Cys | Thr | His | Phe | Pro | Leu | Ile | Ala | His | Gln | Ile | Glu | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| ggc | tat | ttt | atg | gag | cat | ttt | gcc | ctt | tca | acg | ccc | ccc | cta | ctc | atc | 624 | |
| Gly | Tyr | Phe | Met | Glu | His | Phe | Ala | Leu | Ser | Thr | Pro | Pro | Leu | Leu | Ile | | |
| | | | 195 | | | | 200 | | | | | 205 | | | | | |
| cat | tct | ggc | gat | gct | att | gtg | gaa | tat | ttg | caa | caa | aaa | tac | gcc | ctt | 672 | |
| His | Ser | Gly | Asp | Ala | Ile | Val | Glu | Tyr | Leu | Gln | Gln | Lys | Tyr | Ala | Leu | | |
| | | | 210 | | | | 215 | | | | | 220 | | | | | |
| aag | aaa | aac | gca | tgc | gca | ttc | cct | aaa | gta | gaa | ttc | cat | gcg | agc | ggc | 720 | |
| Lys | Lys | Asn | Ala | Cys | Ala | Phe | Pro | Lys | Val | Glu | Phe | His | Ala | Ser | Gly | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| gat | gta | att | tgg | cta | gaa | aaa | cag | gct | aaa | gaa | tgg | ctc | aaa | ttg | taa | 768 | |
| Asp | Val | Ile | Trp | Leu | Glu | Lys | Gln | Ala | Lys | Glu | Trp | Leu | Lys | Leu | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |

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 <213> H. pylori

<400> 30

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Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Gly Glu
 65 70 75 80

Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Arg Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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<221> CDS
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 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30
 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga 192
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
 50 55 60
 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80
 atg caa aag cat tcc aaa atc cct att gtg ggt gtg att gag cca agc 288
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95
 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta 336
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110
 gtg tta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc 384
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125
 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt 432
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140
 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa 480
 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160
 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg 528

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag 576
 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
 180 185 190

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc 624
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

cat tct ggc gat gct att gtg gaa tat ttg caa caa aaa tac acc ctt 672
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
 210 215 220

aag aaa aat gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

gat gtg gtt tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768
 Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

<210> 32
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 <212> PRT
 <213> H. pylori

<400> 32

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu
 1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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 <213> H. pylori

<221> CDS
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 1 5 10 15

aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc 96
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

| | |
|---|-----|
| caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa | 192 |
| Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys | |
| 50 55 60 | |
| tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag | 240 |
| Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu | |
| 65 70 75 80 | |
| atg caa aag cat tcc aaa atc cct gtt gtg ggc gtg att gag cca agc | 288 |
| Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser | |
| 85 90 95 | |
| att tta gcg atc aaa cgg caa gtg aaa gat aaa aac gcc cct att ttg | 336 |
| Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu | |
| 100 105 110 | |
| gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gat aac gcc | 384 |
| Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala | |
| 115 120 125 | |
| ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt | 432 |
| Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu | |
| 130 135 140 | |
| ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa | 480 |
| Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu | |
| 145 150 155 160 | |
| act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg | 528 |
| Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val | |
| 165 170 175 | |
| gtt att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag | 576 |
| Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu | |
| 180 185 190 | |
| ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc | 624 |
| Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile | |
| 195 200 205 | |
| cat tct ggc gat gct att gtg gaa tat ttg caa caa aat tac gcc ctt | 672 |
| His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu | |
| 210 215 220 | |
| aag aaa aac gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc | 720 |
| Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly | |
| 225 230 235 240 | |
| gat gtg gtt tgg cta gaa aaa caa gct aaa gaa tgg ctt aaa ttg | 765 |
| Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu | |
| 245 250 255 | |
| <210> 34 | |
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| <213> H. pylori | |

<400> 34

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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser
 85 90 95

Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
 225 230 235 240

Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu
 245 250 255

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapiens

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<210> 36
 <211> 28
 <212> DNA
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<220>
 <223> Homo sapiens

<400> 36
 agaattctat tacaatttga gccattct 28

<210> 37
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapiens

<400> 37
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<210> 38
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapiens

<400> 38
 ataagtactt gtgaatctta tactag 26

<210> 39
 <211> 858
 <212> DNA
 <213> E. coli

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 cgtcccaccg tgctgggtgtt tgactccggc gtcgggtgggt tgtcgggtcta tgacgagatc 120
 cggcatctct taccggatct ccattacatt tatgctttcg ataacgtcgc tttcccgtat 180
 ggcgaaaaaa gcgaagcgtt tattgttgag cgagtgggtg caattgtcac cgcggtgcaa 240
 gaacgttatc cccttgcgct ggctgtggtc gcttgcaaca ctgccagtac cgtttcactt 300
 cctgcattac gcgaaaagtt cgacttcccg gttgttggtg tcgtgccggc gattaaacct 360
 gctgcacgtc tgacggcaaa tggcattgtc ggattactgg caaccgcgg aacagttaaa 420
 cgttcttata ctcatgagct gatcgcgcgt ttcgctaata aatgccagat agaaatgctg 480
 ggctcggcag agatgggtga gttggctgaa gcgaagctac atggcgaaga tgtttctctg 540
 gatgcactaa aacgtatcct acgcccgtgg ttaagaatga aagagccgcc agataccgtt 600
 gtattgggtt gcacccatct ccctctacta caagaagaac tgttacaagt gctgccagag 660
 ggaacccggc tgggtggattc tggcgcagcg attgctcgcc gaacggcctg gttgttagaa 720
 catgaagccc cggatgcaaa atctgccgat gcgaatattg ccttttgtat ggcaatgacg 780
 ccaggagctg aacaattatt gcccgtttta cagcgttacg gcttcgaaac gctcgaaaaa 840
 ctggcagttt taggctga 858

<210> 40
 <211> 285
 <212> PRT
 <213> E. coli

<400> 40

Met Ala Thr Lys Leu Gln Asp Gly Asn Thr Pro Cys Leu Ala Ala Thr
 1 5 10 15

Pro Ser Glu Pro Arg Pro Thr Val Leu Val Phe Asp Ser Gly Val Gly
 20 25 30

Gly Leu Ser Val Tyr Asp Glu Ile Arg His Leu Leu Pro Asp Leu His
 35 40 45

Tyr Ile Tyr Ala Phe Asp Asn Val Ala Phe Pro Tyr Gly Glu Lys Ser
 50 55 60

Glu Ala Phe Ile Val Glu Arg Val Val Ala Ile Val Thr Ala Val Gln
 65 70 75 80

Glu Arg Tyr Pro Leu Ala Leu Ala Val Val Ala Cys Asn Thr Ala Ser
85 90 95

Thr Val Ser Leu Pro Ala Leu Arg Glu Lys Phe Asp Phe Pro Val Val
100 105 110

Gly Val Val Pro Ala Ile Lys Pro Ala Ala Arg Leu Thr Ala Asn Gly
115 120 125

Ile Val Gly Leu Leu Ala Thr Arg Gly Thr Val Lys Arg Ser Tyr Thr
130 135 140

His Glu Leu Ile Ala Arg Phe Ala Asn Glu Cys Gln Ile Glu Met Leu
145 150 155 160

Gly Ser Ala Glu Met Val Glu Leu Ala Glu Ala Lys Leu His Gly Glu
165 170 175

Asp Val Ser Leu Asp Ala Leu Lys Arg Ile Leu Arg Pro Trp Leu Arg
180 185 190

Met Lys Glu Pro Pro Asp Thr Val Val Leu Gly Cys Thr His Phe Pro
195 200 205

Leu Leu Gln Glu Glu Leu Leu Gln Val Leu Pro Glu Gly Thr Arg Leu
210 215 220

Val Asp Ser Gly Ala Ala Ile Ala Arg Arg Thr Ala Trp Leu Leu Glu
225 230 235 240

His Glu Ala Pro Asp Ala Lys Ser Ala Asp Ala Asn Ile Ala Phe Cys
245 250 255

Met Ala Met Thr Pro Gly Ala Glu Gln Leu Leu Pro Val Leu Gln Arg
260 265 270

Tyr Gly Phe Glu Thr Leu Glu Lys Leu Ala Val Leu Gly
275 280 285

<210> 41

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Homo sapiens

<400> 41

aaatagtcac atgaaaatag gcgtttttg 29

<210> 42

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Homo sapiens

<400> 42

agaattctat tacaatttga gccattct 28

<210> 43

<211> 822

<212> DNA

<213> E. faecalis

<400> 43

atgagcaatc aagaagccat tggattaatt gattctggcg ttggtggatt aactgtttta 60

aaggaagcgc taaagcaatt accaaatgaa cgattaattt atttaggaga tacagcccg 120

tgcccatatg gtccacgacc agccgaacaa gtcgttcagt ttacttggga aatggccgat 180

tttttattga aaaaacgaat aaaaatgcta gtaatcgcat gtaataccgc gacggctgtc 240

gcattagaag aaattaaagc tgccttgcca attccagttg ttggtgttat ttacctggc 300

gcacgagcag ccgttaaagt cacaaaaaat aacaaaattg gtgtcatagg taccttaggg 360

acaatcaaaa gtgcttccta tgaaatcgcc attaaaagta aggcaccagc aattgaggtg 420

actagtttag cttgccctaa atttgtcccc attgttgaaa gtaatcaata tcgttcttcc 480

gtagcaaaaa aaattgtggc agaaacactt caagcactac aattaaaagg acttgatacg 540

ttgatttttag gttgtaccca ttacccggtg ttacgtccgg tgattcaaaa tgtgatgggg 600

agtcatttga cattaattga ctcaggagcc gaaacagttg gcgaagtcag catgcttctc 660

gattattttg acattgcca cagcctgaa gcgcctacac agcccatga atttataca 720

actggttctg caaaaatgtt tgaagagatt gcaagcagtt ggcttggtat agagaactta 780

aaagcacaac agattcactt aggaggaaac gaaaatgatt ag 822

<210> 44

<211> 273

<212> PRT

<213> E. faecalis

<400> 44

Met Ser Asn Gln Glu Ala Ile Gly Leu Ile Asp Ser Gly Val Gly Gly
 1 5 10 15

Leu Thr Val Leu Lys Glu Ala Leu Lys Gln Leu Pro Asn Glu Arg Leu
 20 25 30

Ile Tyr Leu Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro Arg Pro Ala
 35 40 45

Glu Gln Val Val Gln Phe Thr Trp Glu Met Ala Asp Phe Leu Leu Lys
 50 55 60

Lys Arg Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val
 65 70 75 80

Ala Leu Glu Glu Ile Lys Ala Ala Leu Pro Ile Pro Val Val Gly Val
 85 90 95

Ile Leu Pro Gly Ala Arg Ala Ala Val Lys Val Thr Lys Asn Asn Lys
 100 105 110

Ile Gly Val Ile Gly Thr Leu Gly Thr Ile Lys Ser Ala Ser Tyr Glu
 115 120 125

Ile Ala Ile Lys Ser Lys Ala Pro Ala Ile Glu Val Thr Ser Leu Ala
 130 135 140

Cys Pro Lys Phe Val Pro Ile Val Glu Ser Asn Gln Tyr Arg Ser Ser
 145 150 155 160

Val Ala Lys Lys Ile Val Ala Glu Thr Leu Gln Ala Leu Gln Leu Lys
 165 170 175

Gly Leu Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Arg
 180 185 190

Pro Val Ile Gln Asn Val Met Gly Ser His Val Thr Leu Ile Asp Ser
 195 200 205

Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp Tyr Phe Asp
 210 215 220

Ile Ala His Thr Pro Glu Ala Pro Thr Gln Pro His Glu Phe Tyr Thr
 225 230 235 240

Thr Gly Ser Ala Lys Met Phe Glu Glu Ile Ala Ser Ser Trp Leu Gly
 245 250 255

Ile Glu Asn Leu Lys Ala Gln Gln Ile His Leu Gly Gly Asn Glu Asn
 260 265 270

Asp

<210> 45

<211> 801

<212> DNA

<213> S. aureus

<400> 45

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atgaataaac caataggtgt aatagactct ggtgtcggag gtttgacagt agctaaagaa      60
attatgcgtc agttgccaaa tgagacgatt tattacttag gtgatattgg gcgatgtcca      120
tatgggccaa gaccaggaga acaagtaaaa caatatacag ttgaaatcgc tcgtaaatta      180
atggaatttg atataaaaat gctcgtgatt gcttgtaata ctgcaactgc tgtagcttta      240
gaatatttac aaaagacctt atcaatctca gtgattggcg taattgaacc aggtgctaga      300
acagcaataa tgacgactag aaatcaaaaat gtattagtag taggaacgga aggcacaaatt      360
aaatctgaag catatcgaac acatattaaa cgtataaatc cacatgtaga ggtacatggc      420
gttgctgtc cagggtttgt gccacttgta gaacaaatga gatatagtga tccaacaatt      480
acaagcattg ttattcatca aacactgaaa cggtggcgta atagtgagtc tgatactgtc      540
attttaggat gtaccacta tccattgctc tataaaccta tctatgatta ttttggtggg      600
aaaaagacag tgatttcgtc tggattagaa acggctcgtg aagttagtgc attgctaaca      660
tttagtaatg aacatgcaag ttatactgaa catccagatc atcgatTTTT tgcaacaggt      720
gataccacac atattactaa cattatcaaa gaatggctaa atttatctgt caatgtggaa      780
cgtatatcag tgaatgacta g                                     801

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<210> 46

<211> 266

<212> PRT

<213> S. aureus

<400> 46

Met Asn Lys Pro Ile Gly Val Ile Asp Ser Gly Val Gly Gly Leu Thr

| | | | |
|---|-----|-----|-----|
| 1 | 5 | 10 | 15 |
| Val Ala Lys Glu Ile Met Arg Gln Leu Pro Asn Glu Thr Ile Tyr Tyr | 20 | 25 | 30 |
| Leu Gly Asp Ile Gly Arg Cys Pro Tyr Gly Pro Arg Pro Gly Glu Gln | 35 | 40 | 45 |
| Val Lys Gln Tyr Thr Val Glu Ile Ala Arg Lys Leu Met Glu Phe Asp | 50 | 55 | 60 |
| Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu | 65 | 70 | 75 |
| Glu Tyr Leu Gln Lys Thr Leu Ser Ile Ser Val Ile Gly Val Ile Glu | 85 | 90 | 95 |
| Pro Gly Ala Arg Thr Ala Ile Met Thr Thr Arg Asn Gln Asn Val Leu | 100 | 105 | 110 |
| Val Leu Gly Thr Glu Gly Thr Ile Lys Ser Glu Ala Tyr Arg Thr His | 115 | 120 | 125 |
| Ile Lys Arg Ile Asn Pro His Val Glu Val His Gly Val Ala Cys Pro | 130 | 135 | 140 |
| Gly Phe Val Pro Leu Val Glu Gln Met Arg Tyr Ser Asp Pro Thr Ile | 145 | 150 | 155 |
| Thr Ser Ile Val Ile His Gln Thr Leu Lys Arg Trp Arg Asn Ser Glu | 165 | 170 | 175 |
| Ser Asp Thr Val Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Tyr Lys | 180 | 185 | 190 |
| Pro Ile Tyr Asp Tyr Phe Gly Gly Lys Lys Thr Val Ile Ser Ser Gly | 195 | 200 | 205 |
| Leu Glu Thr Ala Arg Glu Val Ser Ala Leu Leu Thr Phe Ser Asn Glu | 210 | 215 | 220 |
| His Ala Ser Tyr Thr Glu His Pro Asp His Arg Phe Phe Ala Thr Gly | 225 | 230 | 235 |
| | | | 240 |

Asp Thr Thr His Ile Thr Asn Ile Ile Lys Glu Trp Leu Asn Leu Ser
 245 250 255

Val Asn Val Glu Arg Ile Ser Val Asn Asp
 260 265

<210> 47
 <211> 822
 <212> DNA
 <213> E. faecium

<400> 47
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 actgtagtaa aagaagccct gaaacaatta ccgaatgaaa atatttttatt tgtaggagac 120
 acagcacgct gcccataatgg ccctagaccc gcggaacagg taatccagta tacttgggaa 180
 atgacggatt atctggtgga gcaaggaatc aagatgctgg tgatcgcctg caataccgca 240
 actgcggtgg ctttagaaga aatcaaagct gctcttttcta ttccagtcac cggtgtgatc 300
 cttcccggta ctagagcggc agtaaaaaaaaa acacaaaata aacaagttgg cattatcggc 360
 acgattggta cggtaaaaaag tcaagcttat gaaaaagcac tgaaagagaa agtaccagaa 420
 ttgactgtga caagtcttgc ttgtccaaaaa tttgttttcag ttgtcgaaag taatgaatac 480
 cattcatcgg tggcgaaaaa aattgtggca gaaacattag ctcctttaac cactaaaaaa 540
 atcgatacat tgatttttggg atgcacccat tatccattat tacgccccat cattcaaaat 600
 gtaatgggag aaaatgttca actgatcgat tctggagcag aaacagtagg tgaagtatct 660
 atgctgttag attatttcaa tctgagcaat tcaccgcaaa atggtcggac attatgccag 720
 ttttatacaa ctggctctgc caaacttttc gaggaatatag ctgaagactg gcttggaatc 780
 ggacacttaa atgtagaaca tatcgaattg ggaggaaaat aa 822

<210> 48
 <211> 273
 <212> PRT
 <213> E. faecium

<400> 48

Met Ile Arg Leu Thr Asp Asn Arg Pro Ile Gly Phe Ile Asp Ser Gly
 1 5 10 15

Val Gly Gly Leu Thr Val Val Lys Glu Ala Leu Lys Gln Leu Pro Asn
 20 25 30

Glu Asn Ile Leu Phe Val Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro
 35 40 45

Arg Pro Ala Glu Gln Val Ile Gln Tyr Thr Trp Glu Met Thr Asp Tyr
 50 55 60

Leu Val Glu Gln Gly Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala
 65 70 75 80

Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Ala Leu Ser Ile Pro Val
 85 90 95

Ile Gly Val Ile Leu Pro Gly Thr Arg Ala Ala Val Lys Lys Thr Gln
 100 105 110

Asn Lys Gln Val Gly Ile Ile Gly Thr Ile Gly Thr Val Lys Ser Gln
 115 120 125

Ala Tyr Glu Lys Ala Leu Lys Glu Lys Val Pro Glu Leu Thr Val Thr
 130 135 140

Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val Glu Ser Asn Glu Tyr
 145 150 155 160

His Ser Ser Val Ala Lys Lys Ile Val Ala Glu Thr Leu Ala Pro Leu
 165 170 175

Thr Thr Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro
 180 185 190

Leu Leu Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu
 195 200 205

Ile Asp Ser Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp
 210 215 220

Tyr Phe Asn Leu Ser Asn Ser Pro Gln Asn Gly Arg Thr Leu Cys Gln
 225 230 235 240

Phe Tyr Thr Thr Gly Ser Ala Lys Leu Phe Glu Glu Ile Ala Glu Asp
 245 250 255

Trp Leu Gly Ile Gly His Leu Asn Val Glu His Ile Glu Leu Gly Gly
 260 265 270

Lys

<210> 49
 <211> 335
 <212> DNA
 <213> E. saccharolyticus

<400> 49
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 gtcgtcgggtg tgatcttacc tgggtactcgt gctgcagtta aagctacgaa aaatcgtcaa 120
 atcgggtatta taggaacagc ggggtacaatt aaaagtagtt cgtatgagca agcaattaaa 180
 atgaaagtgc ctgaagcatc ggtgactagt ttagcttgct ctaaatttgt accgattggt 240
 gaaagtaatc aatttcaatc atcggtagct aaaaaaattg ttgctgagac gttattacca 300
 ttgcaacata aaaaattaga tacgttgatt ttagg 335

<210> 50
 <211> 111
 <212> PRT
 <213> E. saccharolyticus

<400> 50

Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Gln
 1 5 10 15

Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala Ala
 20 25 30

Val Lys Ala Thr Lys Asn Arg Gln Ile Gly Ile Ile Gly Thr Ala Gly
 35 40 45

Thr Ile Lys Ser Ser Ser Tyr Glu Gln Ala Ile Lys Met Lys Val Pro
 50 55 60

Glu Ala Ser Val Thr Ser Leu Ala Cys Pro Lys Phe Val Pro Ile Val
 65 70 75 80

Glu Ser Asn Gln Phe Gln Ser Ser Val Ala Lys Lys Ile Val Ala Glu
 85 90 95

Thr Leu Leu Pro Leu Gln His Lys Lys Leu Asp Thr Leu Ile Leu
 100 105 110

<210> 51
 <211> 344
 <212> DNA
 <213> E. mundtii

<400> 51
 gtaatcgcat gtaataccgc aactgcggtc gcattagaag aaatcaaagc aacactctcg 60
 attccagtga tcggtgtgat tttgccagga acgagagcgg cagtcaagca gacgaaaaat 120
 catcgagtag ggggtgattgg aacaattgg accgtcaaaa gtgctgctta cgagacggca 180
 ttattggata aagcacccga actgaaagtt accagcttgg cgtgtccaaa gtttgtttca 240
 gtcgtagaaa gtaaagaata ccgatcatca gtcgctaaaa aaatcgtggc tcaaactttg 300
 cttccattag aattaaaggg gatcgatacg ttgattttag gttg 344

<210> 52
 <211> 113
 <212> PRT
 <213> E. mundtii

<400> 52

Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys
 1 5 10 15

Ala Thr Leu Ser Ile Pro Val Ile Gly Val Ile Leu Pro Gly Thr Arg
 20 25 30

Ala Ala Val Lys Gln Thr Lys Asn His Arg Val Gly Val Ile Gly Thr
 35 40 45

Ile Gly Thr Val Lys Ser Ala Ala Tyr Glu Thr Ala Leu Leu Asp Lys
 50 55 60

Ala Pro Glu Leu Lys Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser
 65 70 75 80

Val Val Glu Ser Lys Glu Tyr Arg Ser Ser Val Ala Lys Lys Ile Val
 85 90 95

Ala Gln Thr Leu Leu Pro Leu Glu Leu Lys Gly Ile Asp Thr Leu Ile
 100 105 110

Leu

<210> 53

<211> 340
 <212> DNA
 <213> E. casseliflavus

<400> 53
 atcgcgatgta ataccgcgac agcggtcgcc cttgaagaaa tcaaagaaca actaacgatc 60
 ccagtgatcg gcgtgatcct gcctggcagt cgagcagcag tcaaagcaag caaaaaccaa 120
 cgaatcgggtg tcatcgggac aaacggaacg atcaaaagtg actccttaca gcgcgcgctt 180
 catggcaaag cgcccatgc gtccgtcgtc agtttggctt gcccgagtt tgtgccgatc 240
 gtagaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300
 ccattgaaaa acaaacggct agatacgttg attttaggtg 340

<210> 54
 <211> 112
 <212> PRT
 <213> E. casseliflavus

<400> 54
 Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu
 1 5 10 15
 Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala
 20 25 30
 Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn
 35 40 45
 Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala
 50 55 60
 Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
 65 70 75 80
 Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala
 85 90 95
 Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu
 100 105 110

<210> 55
 <211> 337
 <212> DNA
 <213> E. flavescens

<400> 55

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 ccagtgatcg gcgtgatcct gcctggcagt cgagcagcag tcaaagcaag caaaaaccaa 120
 cgaatcgggtg tcatcggggac aaacggaacg atcaaaagtg actcttataa gcgcgcgctt 180
 catggcaaag cgccccatgc gtccgtcgtc agtttggctt gcccgaaagt tgtgccgatac 240
 gtagaaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300
 ccattgaaaa acaaacggct agatacgttg attttag 337

<210> 56
 <211> 112
 <212> PRT
 <213> E. flavescens

<400> 56

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu
 1 5 10 15

Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala
 20 25 30

Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn
 35 40 45

Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala
 50 55 60

Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
 65 70 75 80

Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala
 85 90 95

Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu
 100 105 110

<210> 57
 <211> 341
 <212> DNA
 <213> E. cecorum

<400> 57

atcgcatgta ataccgcgac tgcagcagct ttaaccctaaa ttaaggaaca attagacatt 60
 ccagttgtcg gtgtgatttt acctggaact agagctgctg tcaaaaatac aaaatcgcaa 120
 cgaattggga ttatcggcac acaaggaacc atccaaagtg gcagttatga acaagccatt 180

ctttctaaag taccgactgc tcaacctgtg agtttagcgt gtcctagatt tgttccgata 240
 gtagaaaagta atcaagcaaa ttcaagtgtg gcaaaaaaaaaa ttgtcgctca aacactacaa 300
 ccgatgacga aaaaaaacat cgatacgttg atttttaggtt g 341

<210> 58
 <211> 112
 <212> PRT
 <213> E. cecorum

<400> 58

Ile Ala Cys Asn Thr Ala Thr Ala Ala Ala Leu Thr Gln Ile Lys Glu
 1 5 10 15

Gln Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala
 20 25 30

Ala Val Lys Asn Thr Lys Ser Gln Arg Ile Gly Ile Ile Gly Thr Gln
 35 40 45

Gly Thr Ile Gln Ser Gly Ser Tyr Glu Gln Ala Ile Leu Ser Lys Val
 50 55 60

Pro Thr Ala Gln Pro Val Ser Leu Ala Cys Pro Arg Phe Val Pro Ile
 65 70 75 80

Val Glu Ser Asn Gln Ala Asn Ser Ser Val Ala Lys Lys Ile Val Ala
 85 90 95

Gln Thr Leu Gln Pro Met Thr Lys Lys Asn Ile Asp Thr Leu Ile Leu
 100 105 110

<210> 59
 <211> 339
 <212> DNA
 <213> E. raffinosus

<400> 59

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 cgcgtgggaa ttatcggaac cattggaaca gtaaaaagtgtgttcttataa acacgaacta 180
 caggaaaaag ctcttgatac ttatgttttct agtttagcat gcccaaaatt tgtaccgatt 240
 gttgaaagta atcaatttaa tagctcggtg gcgaaaaaaaaa ttgttttctca aacattaact 300

cctttgaaaa aggaaaagtt ggatacgttg atttttaggt

339

<210> 60
 <211> 112
 <212> PRT
 <213> E. raffinosus

<400> 60

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Arg
 1 5 10 15

Thr Val Asp Ile Pro Val Ile Gly Val Ile Gln Pro Gly Ser Arg Ala
 20 25 30

Ala Leu Lys Ala Ser Glu Asn Gly Arg Val Gly Ile Ile Gly Thr Ile
 35 40 45

Gly Thr Val Lys Ser Gly Ser Tyr Lys His Glu Leu Gln Glu Lys Ala
 50 55 60

Pro Asp Thr Tyr Val Ser Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
 65 70 75 80

Val Glu Ser Asn Gln Phe Asn Ser Ser Val Ala Lys Lys Ile Val Ser
 85 90 95

Gln Thr Leu Thr Pro Leu Lys Lys Glu Lys Leu Asp Thr Leu Ile Leu
 100 105 110

<210> 61
 <211> 341
 <212> DNA
 <213> E. malodoratus

<400> 61

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cctgttattg gtgttatcca accaggatca cgtgctgcat taaaagcaag taaaaatagt 120

cgtgtaggta tcatcggaac actaggaact gttaaaagtg gatcttataa acatgagctg 180

caagaaaaag caccagaaac gtatgttgct agtctggcct gcccaaaatt tgtgccaatc 240

gttgaaagta atcagtttaa tagttctgta gccaaaaaga ttgtttcaca atctctggca 300

cccttaaaaa aggaaaaatt agatacgttg atttttaggtt g 341

<210> 62
 <211> 112
 <212> PRT

<213> E. malodoratus

<400> 62

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Lys
1 5 10 15

Asn Val Asp Ile Pro Val Ile Gly Val Ile Gln Pro Gly Ser Arg Ala
20 25 30

Ala Leu Lys Ala Ser Lys Asn Ser Arg Val Gly Ile Ile Gly Thr Leu
35 40 45

Gly Thr Val Lys Ser Gly Ser Tyr Lys His Glu Leu Gln Glu Lys Ala
50 55 60

Pro Glu Thr Tyr Val Ala Ser Leu Ala Cys Pro Lys Phe Val Pro Ile
65 70 75 80

Val Glu Ser Asn Gln Phe Asn Ser Ser Val Ala Lys Lys Ile Val Ser
85 90 95

Gln Ser Leu Ala Pro Leu Lys Lys Glu Lys Leu Asp Thr Leu Ile Leu
100 105 110

<210> 63

<211> 338

<212> DNA

<213> E. solitarus

<400> 63

gcatgtaata cgcgaacagc tgtggcttta gatgagatta aagagcaact gcaaattccct 60

gttggtggag ttattatgcc gggaaccaga gcagctgtta aagcgactaa aaatcatcgt 120

attggtgtga ttggcacaaa aggaacagtt aaaagtgcct cttacaaacg agcaatcaaa 180

gaaaaaaatg aaaatacaaa agtaacaagt ttggcttgct cgaagtttgt tcccattgtg 240

gaaagtaatc aaattcattc ttcagtggca aaaaaaattg tatttgaaac actattaccc 300

ttaaaaaata aacatttaga tacgttgatt ttaggttg 338

<210> 64

<211> 111

<212> PRT

<213> E. solitarus

<400> 64

Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Asp Glu Ile Lys Glu Gln

| | | | |
|-------------|---------------------|---------------------|---------------------|
| 1 | 5 | 10 | 15 |
| Leu Gln Ile | Pro Val Val Gly Val | Ile Met Pro Gly Thr | Arg Ala Ala |
| | 20 | 25 | 30 |
| Val Lys Ala | Thr Lys Asn His | Arg Ile Gly Val | Ile Gly Thr Lys Gly |
| | 35 | 40 | 45 |
| Thr Val Lys | Ser Ala Ser Tyr | Lys Arg Ala Ile | Lys Glu Lys Asn Glu |
| | 50 | 55 | 60 |
| Asn Thr Lys | Val Thr Ser Leu | Ala Cys Pro Lys | Phe Val Pro Ile Val |
| | 65 | 70 | 75 |
| Glu Ser Asn | Gln Ile His Ser | Ser Val Ala Lys | Lys Ile Val Phe Glu |
| | 85 | 90 | 95 |
| Thr Leu Leu | Pro Leu Lys Asn | Lys His Leu Asp | Thr Leu Ile Leu |
| | 100 | 105 | 110 |

<210> 65
 <211> 341
 <212> DNA
 <213> E. hirae

<400> 65
 atcgcatgta ataccgctac tgcggttgct ttagaagaaa tcaaggcggc acttcctatt 60
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 caagtaggga ttatcggaac cctcggaacg atcaaaagtc gtgcttatga aacagcgctg 180
 aaaacgaagg tacctgaact tgccgtgact agtttggtt gtccaaaatt cgtttcggta 240
 gtggaaagta atgaatatca ttcgtcagtg gcaaaaaaaaa tcgttgccca gacactagcg 300
 ccattgggta ctaagaaaat cgatacggtg attttaggtt g 341

<210> 66
 <211> 111
 <212> PRT
 <213> E. hirae

<400> 66

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|-----|
| Ala Cys Asn | Thr Ala Thr | Ala Val Ala | Leu Glu Glu | Ile Lys Ala | Ala |
| 1 | 5 | 10 | 15 | | |

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|-----|
| Leu Pro Ile | Pro Val Ile | Gly Val Ile | Leu Pro Gly | Thr Arg Ala | Ala |
| 20 | 25 | 30 | | | |

Val Lys Gln Thr Arg Asn Lys Gln Val Gly Ile Ile Gly Thr Leu Gly
 35 40 45

Thr Ile Lys Ser Arg Ala Tyr Glu Thr Ala Leu Lys Thr Lys Val Pro
 50 55 60

Glu Leu Ala Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val
 65 70 75 80

Glu Ser Asn Glu Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala Gln
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Thr Leu Ala Pro Leu Val Thr Lys Lys Ile Asp Thr Leu Ile Leu
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<400> 67
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29

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26

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<213> Aquifex pyrophilus NA sequence

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aatagataca gaaaggttga tatagtatac ctcggtgata ccgcaaggggt tccctacggc 120

ataaggtcta aagatacgat aatcagatac tcccttgagt gtgcgggctt tttaaaggat 180

aagggtgttg atataatcgt cgttgcctgc aataccgcaa gtgcttacgc tcttgaacgt 240

ttaaagaaaag agataaacgt tcccgttttc ggcgttattg aaccgggggt taaagaagcc 300

ttaaaaaagt caaggaataa aaaaatagga gttataggaa ctctgcaac cgtaaaaagc 360

ggagcctacc agagaaagct tgaagagggg ggagctgatg tttttgcaaa ggcctgtccc 420

ctattcgttc cccttgcgga ggaaggtctc cttgaggggg agataacaag aaaggttgta 480

gaacactacc ttaaggagtt taaaggtaag attgatactc tgattttagg atgtacccat 540

tacccccttc ttaaaaagga gataaagaag tttttgggag acgttgaagt cgttgactct 600

tccgaagccc tttcccttc cctccataac tttataaagg acgatgggtc ctcatccctt 660

gagttatttt ttacggacct ttccccaaat ctccagtttt tgattaaatt aatactcggg 720

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<213> Aquifex pyrophilus amino acid sequence

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Lys Ala Ile Arg Asn Arg Tyr Arg Lys Val Asp Ile Val Tyr Leu Gly
20 25 30

Asp Thr Ala Arg Val Pro Tyr Gly Ile Arg Ser Lys Asp Phe Thr Thr
35 40 45

Ile Ile Arg Tyr Ser Leu Glu Cys Ala Gly Phe Leu Lys Asp Lys Gly
50 55 60

Val Asp Ile Ile Val Val Ala Cys Asn Thr Ala Ser Ala Tyr Ala Leu
65 70 75 80

Glu Arg Leu Lys Lys Glu Ile Asn Val Pro Val Phe Gly Val Ile Glu
85 90 95

Pro Gly Val Lys Glu Ala Leu Lys Lys Ser Phe Thr Arg Asn Lys Lys
100 105 110

Ile Gly Val Ile Gly Thr Pro Ala Thr Val Lys Ser Gly Ala Tyr Gln
115 120 125

Arg Lys Leu Glu Glu Gly Gly Ala Asp Val Phe Ala Lys Ala Cys Pro
130 135 140

Leu Phe Val Pro Leu Ala Glu Glu Gly Leu Leu Glu Gly Glu Ile Thr
145 150 155 160

Arg Lys Val Val Glu His Tyr Phe Thr Leu Lys Glu Phe Lys Gly Lys
165 170 175

Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Lys Lys

180

185

190

Glu Ile Lys Lys Phe Leu Gly Asp Val Glu Val Val Asp Ser Ser Glu
 195 200 205

Ala Leu Ser Leu Ser Leu His Asn Phe Ile Lys Asp Asp Gly Ser Ser
 210 215 220

Ser Leu Glu Leu Phe Thr Phe Phe Thr Asp Leu Ser Pro Asn Leu Gln
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Phe Leu Ile Lys Leu Ile Leu Gly Arg Asp Tyr Pro Val Lys Leu Ala
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Glu Gly Val Phe Thr His
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